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TECH CENTER 1600/2900

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/402,845

DATE: 06/21/2001
 TIME: 11:53:55

Input Set : A:\7636-0013.10-seqlist.txt
 Output Set: N:\CRF3\06202001\I402845.raw

SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Laus, Reiner
 6 Ruegg, Curtis L.
 7 Shapero, Michael H.
 8 Yang, Demao
 10 (ii) TITLE OF INVENTION: Composition and Method for
 11 Producing an Immune Response Against Tumor-Related
 Antigens
 13 (iii) NUMBER OF SEQUENCES: 11
 15 (iv) CORRESPONDENCE ADDRESS:
 16 (A) ADDRESSEE: Iota Pi Law Group
 17 (B) STREET: P.O. Box 60850
 18 (C) CITY: Palo Alto
 19 (D) STATE: CA
 20 (E) COUNTRY: US
 21 (F) ZIP: 94306
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Diskette
 25 (B) COMPUTER: IBM Compatible
 26 (C) OPERATING SYSTEM: DOS
 27 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 29 (vi) CURRENT APPLICATION DATA:
 C--> 30 (A) APPLICATION NUMBER: US/09/402,845
 C--> 31 (B) FILING DATE: 04-Oct-1998
 32 (C) CLASSIFICATION:
 34 (vii) PRIOR APPLICATION DATA:
 35 (A) APPLICATION NUMBER: US 60/043,301
 36 (B) FILING DATE: 11-APR-1997
 39 (viii) ATTORNEY/AGENT INFORMATION:
 40 (A) NAME: Dehlinger, Peter J.
 41 (B) REGISTRATION NUMBER: 28,006
 42 (C) REFERENCE/DOCKET NUMBER: 7636-0013.10
 44 (ix) TELECOMMUNICATION INFORMATION:
 45 (A) TELEPHONE: 650-324-0880
 46 (B) TELEFAX: 650-324-0960
 49 (2) INFORMATION FOR SEQ ID NO: 1:
 51 (i) SEQUENCE CHARACTERISTICS:
 52 (A) LENGTH: 1158 base pairs
 53 (B) TYPE: nucleic acid
 54 (C) STRANDEDNESS: single
 55 (D) TOPOLOGY: linear
 57 (ii) MOLECULE TYPE: cDNA
 58 (vi) ORIGINAL SOURCE:
 59 (C) INDIVIDUAL ISOLATE: mouse prostatic acid phosphatase (mPAP)
 61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 63 ATGGGAGCCG TTCCTCTGCC CCTGAGCCCG ACAGCAAGCC TCAGCCTTGG CTTCTTGCTC 60
 64 CTGCTTTTCTC TCTGCCTGGA CCCAGGCCAA GCCAAGGAGT TGAAGTTTGT GACATTGGTG 120

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65  TTTCGACATG GAGACCGAGG TCCCATCGAG ACCTTTCCTA CCGACCCCAT TACGGAATCC      180
66  TCGTGGCCAC AAGGATTTGG CCAACTCACC CAGTGGGGCA TGGAACAGCA CTACGAACTT      240
67  GGAAGTTATA TAAGGAAAAG ATACGGAAGA TTCTTGAACG ACACCTATAA GCATGATCAG      300
68  ATTTATATCC GGAGCACAGA TGTGGACAGG ACTTTGATGA GTGCTATGAC AAACCTTGCA      360
69  GCCCTGTTTC CTCCAGAGGG GATCAGCATC TGGAATCCTA GACTGCTCTG GCAGCCCATC      420
70  CCAGTGCACA CCGTGTCTCT CTCTGAGGAT CGGTTGCTGT ACCTGCCTTT CAGAGACTGC      480
71  CCTCGTTTTG AAGAACTCAA GAGTGAGACT TTAGAATCTG AGGAATTCTT GAAGAGGCTT      540
72  CATCCATATA AAAGCTTCCT GGACACCTTG TCGTCGCTGT CGGGATTCTG TGACCAGGAT      600
73  CTTTTTGGA TCTGGAGTAA AGTTTATGAC CTTTTATTCT GCGAGAGTGT TCACAATTTT      660
74  ACCTTGCCCT CCTGGGCCAC CGAGGACGCC ATGATTAAGT TGAAAGAGCT ATCAGAATTA      720
75  TCTCTGCTAT CACTTTATGG AATTCACAAG CAGAAAGAGA AATCTCGACT CCAAGGGGGC      780
76  GTCCTGGTCA ATGAAATCCT CAAGAATATG AAGCTTGCAA CTCAGCCACA GAAGTATAAA      840
77  AAGCTGGTCA TGTATTCCGC ACACGACACT ACCGTGAGTG GCCTGCAGAT GGCGCTAGAT      900
78  GTTTATAATG GAGTTCTGCC TCCCTACGCT TCTTGCCACA TGATGGAATT GTACCATGAT      960
79  AAGGGGGGGC ACTTTGTGGA GATGTACTAT CGGAATGAGA CCCAGAACGA GCCCTACCCA      1020
80  CTCACGCTGC CAGGCTGCAC CCACAGCTGC CCTCTGGAGA AGTTTGCGGA GCTACTGGAC      1080
81  CCGGTGATCC CBCAGGACTG GGCCACGGAG TGTATGGCCA CAAGCAGCCA CCAAGGTACT      1140
82  GTGGGCGCTT TGGGTTAG                                     1158

```

84 (2) INFORMATION FOR SEQ ID NO: 2:

86 (i) SEQUENCE CHARACTERISTICS:

87 (A) LENGTH: 385 amino acids

88 (B) TYPE: amino acid

89 (D) TOPOLOGY: linear

91 (vi) ORIGINAL SOURCE:

C--> 92 (C) INDIVIDUAL ISOLATE: mouse prostatic acid phosphatase (mPAP)
 93 coding sequence

95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

97 Met Gly Ala Val Pro Leu Pro Leu Ser Pro Thr Ala Ser Leu Ser Leu
98 1 5 10 15
99 Gly Phe Leu Leu Leu Leu Ser Leu Cys Leu Asp Pro Gly Gln Ala Lys
100 20 25 30
101 Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Gly Pro
102 35 40 45
103 Ile Glu Thr Phe Pro Thr Asp Pro Ile Thr Glu Ser Ser Trp Pro Gln
104 50 55 60
105 Gly Phe Gly Gln Leu Thr Gln Trp Gly Met Glu Gln His Tyr Glu Leu
106 65 70 75 80
107 Gly Ser Tyr Ile Arg Lys Arg Tyr Gly Arg Phe Leu Asn Asp Thr Tyr
108 85 90 95
109 Lys His Asp Gln Ile Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr Leu
110 100 105 110
111 Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly Ile
112 115 120 125
113 Ser Ile Trp Asn Pro Arg Leu Leu Trp Gln Pro Ile Pro Val His Thr
114 130 135 140
115 Val Ser Leu Ser Glu Asp Arg Leu Leu Tyr Leu Pro Phe Arg Asp Cys
116 145 150 155 160
117 Pro Arg Phe Glu Glu Leu Lys Ser Glu Thr Leu Glu Ser Glu Glu Phe
118 165 170 175

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119 Leu Lys Arg Leu His Pro Tyr Lys Ser Phe Leu Asp Thr Leu Ser Ser .
120           180           185           190
121 Leu Ser Gly Phe Asp Asp Gln Asp Leu Phe Gly Ile Trp Ser Lys Val
122           195           200           205
123 Tyr Asp Pro Leu Phe Cys Glu Ser Val His Asn Phe Thr Leu Pro Ser
124           210           215           220
125 Trp Ala Thr Glu Asp Ala Met Ile Lys Leu Lys Glu Leu Ser Glu Leu
126           225           230           235           240
127 Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser Arg
128           245           250           255
129 Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Lys Asn Met Lys Leu
130           260           265           270
131 Ala Thr Gln Pro Gln Lys Tyr Lys Lys Leu Val Met Tyr Ser Ala His
132           275           280           285
133 Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn Gly
134           290           295           300
135 Val Leu Pro Pro Tyr Ala Ser Cys His Met Met Glu Leu Tyr His Asp
136           305           310           315           320
137 Lys Gly Gly His Phe Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln Asn
138           325           330           335
139 Glu Pro Tyr Pro Leu Thr Leu Pro Gly Cys Thr His Ser Cys Pro Leu
140           340           345           350
141 Glu Lys Phe Ala Glu Leu Leu Asp Pro Val Ile Pro Gln Asp Trp Ala
142           355           360           365
143 Thr Glu Cys Met Ala Thr Ser Ser His Gln Gly Thr Val Gly Ala Leu
144           370           375           380
145 Gly
146 385

```

148 (2) INFORMATION FOR SEQ ID NO: 3:

150 (i) SEQUENCE CHARACTERISTICS:

151 (A) LENGTH: 22 base pairs

152 (B) TYPE: nucleic acid

153 (C) STRANDEDNESS: single

154 (D) TOPOLOGY: linear

156 (vi) ORIGINAL SOURCE:

157 (C) INDIVIDUAL ISOLATE: gene specific primer for 5' end cloning
 158 of mPAP from mouse prostate (first round)

160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

162 CATTCCGGTA GTACATCTCC AC

22

164 (2) INFORMATION FOR SEQ ID NO: 4:

166 (i) SEQUENCE CHARACTERISTICS:

167 (A) LENGTH: 22 base pairs

168 (B) TYPE: nucleic acid

169 (C) STRANDEDNESS: single

170 (D) TOPOLOGY: linear

172 (vi) ORIGINAL SOURCE:

173 (C) INDIVIDUAL ISOLATE: gene specific primer for 5' end cloning
 174 of mPAP from mouse prostate (second round)

176 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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178 GTCACAAACT TCAACTCCTT GG                                22
180 (2) INFORMATION FOR SEQ ID NO: 5:
182   (i) SEQUENCE CHARACTERISTICS:
183       (A) LENGTH: 21 base pairs
184       (B) TYPE: nucleic acid
185       (C) STRANDEDNESS: single
186       (D) TOPOLOGY: linear
188   (vi) ORIGINAL SOURCE:
189       (C) INDIVIDUAL ISOLATE: gene specific primer for 3' end cloning
190                               of mPAP from mouse prostate (first round)
192   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:                                21
194 GATGTACTAC CGGAATGAGA C
196 (2) INFORMATION FOR SEQ ID NO: 6:
198   (i) SEQUENCE CHARACTERISTICS:
199       (A) LENGTH: 19 base pairs
200       (B) TYPE: nucleic acid
201       (C) STRANDEDNESS: single
202       (D) TOPOLOGY: linear
204   (vi) ORIGINAL SOURCE:
205       (C) INDIVIDUAL ISOLATE: gene specific primer for 3' end cloning
206                               of mPAP from mouse prostate (second round)
208   (ix) FEATURE:
213       (A) NAME/KEY: Other
211       (B) LOCATION: 1, 10
212       (D) OTHER INFORMATION: \note: "where N is A, G, C, or T"
217   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:                                19
219 NGTGATCCCN CARGACTGG
221 (2) INFORMATION FOR SEQ ID NO: 7:
223   (i) SEQUENCE CHARACTERISTICS:
224       (A) LENGTH: 27 base pairs
225       (B) TYPE: nucleic acid
226       (C) STRANDEDNESS: single
227       (D) TOPOLOGY: linear
229   (vi) ORIGINAL SOURCE:
230       (C) INDIVIDUAL ISOLATE: synthetic anchor primer one (AP1) for
231                               mPAP cloning
233   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:                                27
235 CCATCCTAAT ACGACTCACT ATAGGGC
237 (2) INFORMATION FOR SEQ ID NO: 8:
239   (i) SEQUENCE CHARACTERISTICS:
240       (A) LENGTH: 23 base pairs
241       (B) TYPE: nucleic acid
242       (C) STRANDEDNESS: single
243       (D) TOPOLOGY: linear
245   (vi) ORIGINAL SOURCE:
246       (C) INDIVIDUAL ISOLATE: synthetic anchor primer two (AP2) for
247                               mPAP cloning
249   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
251 ACTCACTATA GGGCTCGAGC GGC                                23

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253 (2) INFORMATION FOR SEQ ID NO: 9:
255     (i) SEQUENCE CHARACTERISTICS:
256         (A) LENGTH: 20 base pairs
257         (B) TYPE: nucleic acid
258         (C) STRANDEDNESS: single
259         (D) TOPOLOGY: linear
261     (vi) ORIGINAL SOURCE:
262         (C) INDIVIDUAL ISOLATE: forward primer (A31091) for mPAP
263             amplification
265     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
267     AAGTGCAGCA CCTCCTAAGG                                     20
269 (2) INFORMATION FOR SEQ ID NO: 10:
271     (i) SEQUENCE CHARACTERISTICS:
272         (A) LENGTH: 19 base pairs
273         (B) TYPE: nucleic acid
274         (C) STRANDEDNESS: single
275         (D) TOPOLOGY: linear
277     (vi) ORIGINAL SOURCE:
278         (C) INDIVIDUAL ISOLATE: reverse primer (A31093) for mPAP
279             amplification
281     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
283     GCACTTCCTG CTGAGCTCC                                     19
285 (2) INFORMATION FOR SEQ ID NO: 11:
287     (i) SEQUENCE CHARACTERISTICS:
288         (A) LENGTH: 31 amino acids
289         (B) TYPE: amino acid
290         (D) TOPOLOGY: linear
292     (vi) ORIGINAL SOURCE:
293         (C) INDIVIDUAL ISOLATE: signal peptide of the deduced amino
294             acid sequence for mPAP
296     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
298     Met Gly Ala Val Pro Leu Pro Leu Ser Pro Thr Ala Ser Leu Ser Leu
299     1      5      10      15
300     Gly Phe Leu Leu Leu Ser Leu Cys Leu Asp Pro Gly Gln Ala
301     20      25      30

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VERIFICATION SUMMARY

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TIME: 11:53:56

Input Set : A:\7636-0013.10-seqlist.txt

Output Set: N:\CRF3\06202001\I402845.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:92 M:220 C: Keyword misspelled or invalid format, [(C) INDIVIDUAL ISOLATE:]